

M. Branmock

#10  
7/27P  
1646

RAW SEQUENCE LISTING                      DATE: 06/21/2000  
PATENT APPLICATION:    US/09/380,682              TIME: 10:45:18

Input Set : A:\Jpi-107.app  
Output Set: N:\CRF3\06212000\I380682.raw

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SEQUENCE LISTING

4 (1) GENERAL INFORMATION:  
6     (i) APPLICANT: MOSSAKOWSKA, Danuta Ewa Irena  
7                      COX, Vivienne Frances  
8                      SMITH, Richard Anthony Godwin  
10    (ii) TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE  
11                      SEQUENCES  
13    (iii) NUMBER OF SEQUENCES: 64  
15    (iv) CORRESPONDENCE ADDRESS:  
16          (A) ADDRESSEE: FOLEY & LARDNER  
17          (B) STREET: 3000 K Street, N.W.  
18          (C) CITY: Washington  
19          (D) STATE: D.C.  
20          (E) COUNTRY: U.S.A.  
21          (F) ZIP: 20007-5109  
23    (v) COMPUTER READABLE FORM:  
24          (A) MEDIUM TYPE: Floppy disk  
25          (B) COMPUTER: IBM PC compatible  
26          (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
27          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
C--> 29    (vi) CURRENT APPLICATION DATA:  
C--> 30          (A) APPLICATION NUMBER: US/09/380,682  
C--> 31          (B) FILING DATE: 19-Oct-1999  
32          (C) CLASSIFICATION:  
38    (vii) PRIOR APPLICATION DATA:  
35          (A) APPLICATION NUMBER: WO PCT/GB98/00727  
36          (B) FILING DATE: 05-MAR-1998  
39          (A) APPLICATION NUMBER: GB 9704519.9  
40          (B) FILING DATE: 05-MAR-1997  
42    (viii) ATTORNEY/AGENT INFORMATION:  
43          (A) NAME: ISACSON, John P.  
44          (B) REGISTRATION NUMBER: 33,715  
45          (C) REFERENCE/DOCKET NUMBER: 88362/107  
47    (ix) TELECOMMUNICATION INFORMATION:  
48          (A) TELEPHONE: (202) 672-5300  
49          (B) TELEFAX: (202) 672-5399  
52 (2) INFORMATION FOR SEQ ID NO: 1:  
54    (i) SEQUENCE CHARACTERISTICS:  
55          (A) LENGTH: 197 amino acids  
56          (B) TYPE: amino acid  
57          (C) STRANDEDNESS:  
58          (D) TOPOLOGY: linear  
60    (ii) MOLECULE TYPE: peptide  
65    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
67    Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn  
68    1                      5                      10                      15  
70    Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu

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71          20          25          30
73      Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
74          35          40          45
76      Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
77          50          55          60
79      Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
80          65          70          75          80
82      Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
83          85          90          95
85      Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
86          100          105          110
88      Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
89          115          120          125
91      Pro Pro Thr Ile Ala Asn Gly Asp Phe Thr Ser Ile Ser Arg Glu Tyr
92          130          135          140
94      Phe His Tyr Gly Ser Val Val Thr Tyr His Cys Asn Leu Gly Ser Arg
95          145          150          155          160
97      Gly Lys Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
98          165          170          175
100      Ser Lys Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
101          180          185          190
103      Ile Ile Pro Asn Lys
104          195
106 (2) INFORMATION FOR SEQ ID NO: 2:
108     (i) SEQUENCE CHARACTERISTICS:
109         (A) LENGTH: 591 base pairs
110         (B) TYPE: nucleic acid
111         (C) STRANDEDNESS: single
112         (D) TOPOLOGY: linear
114     (ii) MOLECULE TYPE: DNA (genomic)
119     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
121 ATGCAGTGCA ACGCTCCGGA ATGGCTGCCG TTCGCGCGCC CGACCAACCT GACTGATGAA      60
123 TTTGAGTTCC CGATCGGTAC CTACCTGAAC TACGAATGCC GCCCGGGTTA TAGCGGCCGC      120
125 CCGTTTCTTA TCATCTGCCT GAAAAACTCT GTCTGGACTG GTGCTAAGGA CCGTTGCCGA      180
127 CGTAAATCTT GTCGTAATCC GCCAGATCCG GTTAACGGCA TGGTGCATGT GATCAAAGGC      240
129 ATCCAGTTCG GTTCCCAAAAT TAAATATTCT TGTACTAAAG GTTACCGTCT GATTGGTTCC      300
131 TCCAGCGCTA CATGCATCAT CTCTGGTGAT ACTGTCATTT GGGATAATGA AACACCGATT      360
133 TGTGACCGAA TTCCGTGTGG TCTGCCGCGG ACCATCGCCA ACGGTGATTT CACCTCTATC      420
135 AGTCGCGAGT ATTTTCACTA TGGTTCTGTG GTGACCTACC ACTGCAATCT GGGTAGCCGT      480
137 GGTA AAAAGG TGTTTGAGCT CGTGGGTGAG CCGTCCATCT ACTGCACTAG CAAAGACGAT      540
139 CAAGTGGGCA TCTGGAGCGG CCCGGCACCG CAGTGCATCA TCCCGAACAA A      591
141 (2) INFORMATION FOR SEQ ID NO: 3:
143     (i) SEQUENCE CHARACTERISTICS:
144         (A) LENGTH: 50 base pairs
145         (B) TYPE: nucleic acid
146         (C) STRANDEDNESS: single
147         (D) TOPOLOGY: linear
149     (ii) MOLECULE TYPE: DNA (genomic)
154     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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156 CGACCATCGC CAACGGTGAT TTCACCTCTA TCAGTCGCGA GTATTTTCAC 50  
 158 (2) INFORMATION FOR SEQ ID NO: 4:  
 160 (i) SEQUENCE CHARACTERISTICS:  
 161 (A) LENGTH: 50 base pairs  
 162 (B) TYPE: nucleic acid  
 163 (C) STRANDEDNESS: single  
 164 (D) TOPOLOGY: linear  
 166 (ii) MOLECULE TYPE: DNA (genomic)  
 171 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
 173 GTGAAATAC TCGCGACTGA TAGAGGTGAA ATCACCGTTG GCGATGGTCG 50  
 175 (2) INFORMATION FOR SEQ ID NO: 5:  
 177 (i) SEQUENCE CHARACTERISTICS:  
 178 (A) LENGTH: 47 base pairs  
 179 (B) TYPE: nucleic acid  
 180 (C) STRANDEDNESS: single  
 181 (D) TOPOLOGY: linear  
 183 (ii) MOLECULE TYPE: DNA (genomic)  
 188 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 190 GACCTACCAC TGCAATCTGG GTAGCCGTGG TAAAAGGTG TTTGAGC 47  
 192 (2) INFORMATION FOR SEQ ID NO: 6:  
 194 (i) SEQUENCE CHARACTERISTICS:  
 195 (A) LENGTH: 47 base pairs  
 196 (B) TYPE: nucleic acid  
 197 (C) STRANDEDNESS: single  
 198 (D) TOPOLOGY: linear  
 200 (ii) MOLECULE TYPE: DNA (genomic)  
 205 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 207 GCTCAAACAC CTTTTACCA CGGCTACCCA GATTGCAGTG GTAGGTC 47  
 209 (2) INFORMATION FOR SEQ ID NO: 7:  
 211 (i) SEQUENCE CHARACTERISTICS:  
 212 (A) LENGTH: 25 base pairs  
 213 (B) TYPE: nucleic acid  
 214 (C) STRANDEDNESS: single  
 215 (D) TOPOLOGY: linear  
 217 (ii) MOLECULE TYPE: DNA (genomic)  
 222 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 224 GCACTAGCAA AGACGATCAA GTGGG 25  
 226 (2) INFORMATION FOR SEQ ID NO: 8:  
 228 (i) SEQUENCE CHARACTERISTICS:  
 229 (A) LENGTH: 25 base pairs  
 230 (B) TYPE: nucleic acid  
 231 (C) STRANDEDNESS: single  
 232 (D) TOPOLOGY: linear  
 234 (ii) MOLECULE TYPE: DNA (genomic)  
 239 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
 241 CCCACTTGAT CGTCTTGCT AGTGC 25  
 243 (2) INFORMATION FOR SEQ ID NO: 9:  
 245 (i) SEQUENCE CHARACTERISTICS:  
 246 (A) LENGTH: 197 amino acids

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247      (B) TYPE: amino acid
248      (C) STRANDEDNESS:
249      (D) TOPOLOGY: linear
251      (ii) MOLECULE TYPE: peptide
256      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
258      Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
259      1          5          10          15
261      Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
262      20          25          30
264      Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
265      35          40          45
267      Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
268      50          55          60
270      Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
271      65          70          75          80
273      Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
274      85          90          95
276      Leu Ile Gly Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
277      100         105         110
279      Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
280      115         120         125
282      Pro Pro Thr Ile Ala Asn Gly Asp Phe Thr Ser Ile Ser Arg Glu Tyr
283      130         135         140
285      Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
286      145         150         155         160
288      Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
289      165         170         175
291      Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
292      180         185         190
294      Ile Ile Pro Asn Lys
295      195
297      (2) INFORMATION FOR SEQ ID NO: 10:
299      (i) SEQUENCE CHARACTERISTICS:
300          (A) LENGTH: 591 base pairs
301          (B) TYPE: nucleic acid
302          (C) STRANDEDNESS: single
303          (D) TOPOLOGY: linear
305      (ii) MOLECULE TYPE: DNA (genomic)
310      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
312      ATGCAGTGCA ACGCTCCGGA ATGGCTGCCG TTCGCGCGCC CGACCAACCT GACTGATGAA      60
314      TTGAGTTCC CGATCGGTAC CTACCTGAAC TACGAATGCC GCCCGGGTTA TAGCGGCCGC      120
316      CCGTTTCTA TCATCTGCCT GAAAACTCT GTCTGGACTG GTGCTAAGGA CCGTTGCCGA      180
318      CGTAAATCTT GTCGTAATCC GCCAGATCCG GTTAACGGCA TGGTGCATGT GATCAAAGGC      240
320      ATCCAGTTCG GTTCCCAAAT TAAATATTCT TGTACTAAAG GTTACCGTCT GATTGGTTCC      300
322      TCCAGCGCTA CATGCATCAT CTCTGGTGAT ACTGTCATT GGGATAATGA AACACCGATT      360
324      TGTGACCGAA TTCCGTGTGG TCTGCCGCCG ACCATCGCCA ACGGTGATT CACCTCTATC      420
326      AGTCGCGAGT ATTTTCACTA TGGTTCTGTG GTGACCTACC GCTGCAATCC GGGTAGCGGT      480
328      GGTCGTAAGG TGTTTGAGCT CGTGGGTGAG CCGTCCATCT ACTGCACTAG TAATGACGAT      540
330      CAAGTGGGCA TCTGGAGCGG CCCGGCACCG CAGTGCATCA TCCGAACAA A      591

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332 (2) INFORMATION FOR SEQ ID NO: 11:
334 (i) SEQUENCE CHARACTERISTICS:
335 (A) LENGTH: 197 amino acids
336 (B) TYPE: amino acid
337 (C) STRANDEDNESS:
338 (D) TOPOLOGY: linear
340 (ii) MOLECULE TYPE: peptide
345 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
347 Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
348 1 5 10 15
350 Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
351 20 25 30
353 Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
354 35 40 45
356 Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
357 50 55 60
359 Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
360 65 70 75 80
362 Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
363 85 90 95
365 Leu Ile Gly Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
366 100 105 110
368 Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
369 115 120 125
371 Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
372 130 135 140
374 Phe His Tyr Gly Ser Val Val Thr Tyr His Cys Asn Leu Gly Ser Arg
375 145 150 155 160
377 Gly Lys Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
378 165 170 175
380 Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
381 180 185 190
383 Ile Ile Pro Asn Lys
384 195
386 (2) INFORMATION FOR SEQ ID NO: 12:
388 (i) SEQUENCE CHARACTERISTICS:
389 (A) LENGTH: 591 base pairs
390 (B) TYPE: nucleic acid
391 (C) STRANDEDNESS: single
392 (D) TOPOLOGY: linear
394 (ii) MOLECULE TYPE: DNA (genomic)
399 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
401 ATGCAGTGCA ACGCTCCGGA ATGGCTGCCG TTCGCGCGCC CGACCAACCT GACTGATGAA 60
403 TTTGAGTTCC CGATCGGTAC CTACCTGAAC TACGAATGCC GCCCGGGTTA TAGCGGCCGC 120
405 CCGTTTCTTA TCATCTGCCT GAAAACTCT GTCTGGACTG GTGCTAAGGA CCGTTGCCGA 180
407 CGTAAATCTT GTCGTAATCC GCCAGATCCG GTTAACGGCA TGGTGCATGT GATCAAAGGC 240
409 ATCCAGTTCG GTTCCCAAAT TAAATATTCT TGTACTAAAG GTTACCGTCT GATTGGTTCC 300
411 TCCAGCGCTA CATGCATCAT CTCTGGTGAT ACTGTCATT GGGATAATGA AACACCGATT 360
413 TGTGACCGAA TTCCGTGTGG TCTGCCGCCG ACCATCACCA ACGGTGATTT CATCTCTACC 420

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VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/380,682

DATE: 06/21/2000  
TIME: 10:45:20

Input Set : A:\Jpi-107.app  
Output Set: N:\CRF3\06212000\I380682.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]